## CLAIMS

***This listing of claims replaces all prior versions.***

Claims 1-29. (Canceled)

30. (Currently amended) A method of identifying endogenous mRNA subsets in a cell, comprising the steps of:

(a) lysing a cell comprising an mRNA-protein (mRNP) complex to produce a lysate;

(b) contacting the lysate with an antibody that specifically binds at least one component of the mRNP complex;

(c) partitioning the mRNP complex by capturing the antibody on a solid support;

(d) removing the captured mRNP complex from the lysate; and

(e) identifying a plurality of mRNAs from the mRNP complex without amplifying the mRNAs by PCR, wherein the identified mRNAs are encoded by a plurality of genes.

31. (Previously presented) The method of claim 30, wherein the plurality of mRNAs are reverse transcribed prior to their identification.

32. (Previously presented) The method of claim 30, wherein the plurality of mRNAs are identified by hybridization to known nucleic acid sequences.

33. (Previously presented) The method of claim 30, wherein the plurality of mRNAs are identified by sequencing each mRNA.

34. (Previously presented) The method of claim 32, wherein the plurality of mRNAs are identified using a microarray.

35. (Previously presented) The method of claim 34, wherein the microarray is a cDNA array.

36. (Previously presented) The method of claim 30, wherein the method does not include iterative selection prior to the identification of the mRNAs.

37. (Currently amended) The method of claim 30, wherein the component of the captured mRNP complex to which the antibody binds is an endogenous RNA-binding protein.

38. (Currently amended) The method of claim 37, wherein the endogenous RNA-binding protein is polyA-binding protein (PABP).

~~polyA-binding protein (PABP).~~

39. (Canceled)

40. (Currently amended) The method of claim 30, further comprising identifying ~~changes in~~ the endogenous mRNA subsets following treatment of the cell with a drug to identify changes in the mRNA subsets.

41. (Currently amended) The method of claim 30, further comprising identifying ~~changes in~~ the endogenous mRNA subsets during cell cycle, developmental events, or a state of ~~ageing~~ aging to identify changes in the mRNA subsets.

42. (Previously presented) The method of claim 30, wherein the cell is a tumor cell.

43. (Previously presented) The method of claim 30, wherein the cell is an animal or plant cell.

44. (Previously presented) The method of claim 30, wherein the cell is infected with a pathogen.

45. (Previously presented) The method of claim 30, wherein the RNA-binding protein is tissue-specific.

46. (Previously presented) The method of claim 30, wherein the plurality of mRNAs are identified *en masse*.

47. (Previously presented) The method of claim 30, wherein the plurality of mRNAs comprises approximately 10% of total mRNAs.

48. (Currently amended) A method of identifying endogenous mRNA subsets in a cell, comprising the steps of:

(a) expressing an epitope-tagged RNA-binding protein or an epitope-tagged RNA-associated protein (RAP) ~~ectopically expressed~~ in a cell, thereby forming an mRNP complex;

(b) lysing the cell;

(c) partitioning the mRNP complex by capturing the RNA binding protein or the RAP on a solid support;

(d) removing the captured mRNP complex from the lysate; and

(e) identifying a plurality of mRNAs from the mRNP complex without amplifying the mRNAs by PCR, wherein the identified mRNAs are encoded by a plurality of genes.

49. (Previously presented) The method of claim 48, wherein the plurality of mRNAs are reverse transcribed prior to their identification.

50. (Previously presented) The method of claim 48, wherein the plurality of mRNAs are identified by hybridization to known nucleic acid sequences.

51. (Previously presented) The method of claim 48, wherein the plurality of mRNAs are identified by sequencing each mRNA.

52. (Previously presented) The method of claim 50, wherein the plurality of mRNAs are identified using a microarray.

53. (Previously presented) The method of claim 52, wherein the microarray is a cDNA array.

54. (Previously presented) The method of claim 48, wherein the method does not include iterative selection prior to the identification of the mRNAs.

55. (Currently amended) The method of claim 48, wherein the epitope-tagged RNA-binding protein [[is]] comprises ELAV/Hu protein.

56. (Currently amended) The method of claim 55, wherein the epitope-tagged RNA-binding protein [[is]] comprises HuA or HuB.

57. (Previously presented) The method of claim 48, wherein the epitope tag is a bacteriophage gene-10 tag.

58. (Previously presented) The method of claim 48, wherein the mRNP complex is contacted with the epitope-tagged RNA-binding protein.

59. (Currently amended) The method of claim 48, further comprising identifying ~~changes in~~ the endogenous mRNA subsets following treatment of the cell with a drug to identify changes in the mRNA subsets.

60. (Currently amended) The method of claim 48, further comprising identifying ~~changes in~~ the endogenous mRNA subsets during cell cycle, developmental events, or a state of ~~ageing~~ aging to identify changes in the mRNA subsets.

61. (Previously presented) The method of claim 48, wherein the cell is a tumor cell.

62. (Previously presented) The method of claim 48, wherein the cell is an animal or plant cell.

63. (Previously presented) The method of claim 48, wherein the cell is infected with a pathogen.

64. (Previously presented) The method of claim 48, wherein the RNA-binding protein or the RAP is tissue-specific.

65. (Previously presented) The method of claim 48, wherein the plurality of mRNAs are identified *en masse*.

66. (Previously presented) The method of claim 48, wherein the plurality of mRNAs comprises approximately 10% of total mRNAs.